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RAW SEQUENCE LISTING

DATE: 01/07/2003

PATENT APPLICATION: US/09/756,481D

TIME: 14:07:09

Input Set : A:\47506-sequence.txt

Output Set: N:\CRF4\01072003\I756481D.raw

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3 <110> APPLICANT: MARCHIONNI, MARK
4     JARPE, MICHAEL
5     EBENDAL, TED
7 <120> TITLE OF INVENTION: METHODS FOR TREATING NEUROLOGICAL INJURIES AND
8     DISORDERS
10 <130> FILE REFERENCE: 47506(47843)
12 <140> CURRENT APPLICATION NUMBER: 09/756,481D
13 <141> CURRENT FILING DATE: 2001-01-08
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/15106
16 <151> PRIOR FILING DATE: 1999-07-02
18 <150> PRIOR APPLICATION NUMBER: 60/091,791
19 <151> PRIOR FILING DATE: 1998-07-06
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1387
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus sp.
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (218)..(1288)
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35 cccttctcca gggactctgg ctgccagcag ctccgccttt cagatcaatt ctcgaccacc 60
37 caccttggga ctgccgcca gtcctgccct ctggatcagt ggggtccaga cacgccccct 120
39 ccaggacctc aaagcacccc cgacctaaagg tcaccagccc actggcccca gacgcagtgg 180
41 gctccgctga ctctcttga cacctcctgg gaggaata atg ctc cct gtc tgc cat 235
42                                     Met Leu Pro Val Cys His
43                                     1           5
45 cgt ttt tgc gac cac ctc ctc ctc ctg ctc ttg ctg ccc tcg acg acc 283
46 Arg Phe Cys Asp His Leu Leu Leu Leu Leu Leu Pro Ser Thr Thr
47          10           15           20
49 ctg gcc ccc gcg cca gca tcc atg ggc ccc gct gcc gcc ctg ctc cag 331
50 Leu Ala Pro Ala Pro Ala Ser Met Gly Pro Ala Ala Ala Leu Leu Gln
51          25           30           35
53 gtt ctt ggg ctt ccc gaa gcg ccc cgg agc gtc ccc aca cac cga cct 379
54 Val Leu Gly Leu Pro Glu Ala Pro Arg Ser Val Pro Thr His Arg Pro
55          40           45           50
57 gtg cct cct gtc atg tgg cgc cta ttc cgt cgc cgt gac ccc cag gag 427
58 Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp Pro Gln Glu
59          55           60           65           70
61 gcc aga gtg gga cgc cct ctg cgg cca tgc cac gtg gag gaa cta ggg 475
62 Ala Arg Val Gly Arg Pro Leu Arg Pro Cys His Val Glu Glu Leu Gly
63          75           80           85

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65 gtc gcc gga aac att gtg cgc cac atc ccc gac agc ggt ctg tcc tcc 523
66 Val Ala Gly Asn Ile Val Arg His Ile Pro Asp Ser Gly Leu Ser Ser
67          90          95          100
69 agg ccc gca caa ccc gcc agg acc tcg ggg ctg tgc ccc gag tgg aca 571
70 Arg Pro Ala Gln Pro Ala Arg Thr Ser Gly Leu Cys Pro Glu Trp Thr
71          105          110          115
73 gtc gtc ttt gac ctg tcg aat gtg gag ccc aca gag cgc cca aca cgc 619
74 Val Val Phe Asp Leu Ser Asn Val Glu Pro Thr Glu Arg Pro Thr Arg
75          120          125          130
77 gcg cgc tta gag ttg cgg ctg gag gct gag tgt gaa gat aca gga ggg 667
78 Ala Arg Leu Glu Leu Arg Leu Glu Ala Glu Cys Glu Asp Thr Gly Gly
79 135          140          145          150
81 tgg gag cta agc gtg gca ctg tgg gcc gac gag cat cca ggg cct 715
82 Trp Glu Leu Ser Val Ala Leu Trp Ala Asp Ala Glu His Pro Gly Pro
83          155          160          165
85 gag ctg ctg cgc gtg ccg gcg cca cca ggg gtg ctc ctg cgc gca gac 763
86 Glu Leu Leu Arg Val Pro Ala Pro Pro Gly Val Leu Leu Arg Ala Asp
87          170          175          180
89 cta ctg ggg act gca gta gcc gcc aac gca tca gtg ccc tgt act gtg 811
90 Leu Leu Gly Thr Ala Val Ala Ala Asn Ala Ser Val Pro Cys Thr Val
91          185          190          195
93 cgc ctg gcg ctg tca ctg cac cct ggg gcc act gca gcc tgt ggg cgc 859
94 Arg Leu Ala Leu Ser Leu His Pro Gly Ala Thr Ala Ala Cys Gly Arg
95          200          205          210
97 ctg gct gag gcc tcc ctg ctg ctg gtg acg ctg gac cca cgc ctg tgt 907
98 Leu Ala Glu Ala Ser Leu Leu Leu Val Thr Leu Asp Pro Arg Leu Cys
99 215          220          225          230
101 ccc ttg ccg cga ttg cgg cgc cac acg gag ccc agg gta gaa gtt ggt 955
102 Pro Leu Pro Arg Leu Arg Arg His Thr Glu Pro Arg Val Glu Val Gly
103          235          240          245
105 cca gtg ggc act tgt cgt acc cga cgg ttg cat gtg agc ttc cgt gag 1003
106 Pro Val Gly Thr Cys Arg Thr Arg Arg Leu His Val Ser Phe Arg Glu
107          250          255          260
109 gtg ggc tgg cac cgt tgg gtg atc gcg ccg cgt ggc ttc cta gcc aac 1051
110 Val Gly Trp His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn
111          265          270          275
113 ttc tgc cag ggc acg tgc gca cta ccc gaa acg ctg agg gga ccc ggc 1099
114 Phe Cys Gln Gly Thr Cys Ala Leu Pro Glu Thr Leu Arg Gly Pro Gly
115          280          285          290
117 ggg ccg cct gca ctc aac cac gct gtg ctg cgc gcg ctc atg cac gca 1147
118 Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala
119 295          300          305          310
121 gct gct ccc acc ccg ggt gca ggc tcg ccc tgc tgc gtg cca gag cgt 1195
122 Ala Ala Pro Thr Pro Gly Ala Gly Ser Pro Cys Cys Val Pro Glu Arg
123          315          320          325
125 cta tca ccc atc tcc gtg ctc ttc ttc gac aat agt gac aac gtg gtc 1243
126 Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val
127          330          335          340
129 ctg cga cac tac gaa gac atg gtg gtg gat gag tgt ggc tgc cgt 1288

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130 Leu Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
131      345      350      355
133 tgaccaccccg ggacaccctt tcagggaccg cccacgcaa aagcaggac tgtttgttca 1348
135 tgtttttattg gtgacaaaaa gcttaaaaca aatttgact 1387
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 357
140 <212> TYPE: PRT
141 <213> ORGANISM: Mus sp.
143 <400> SEQUENCE: 2
144 Met Leu Pro Val Cys His Arg Phe Cys Asp His Leu Leu Leu Leu Leu
145 1 5 10 15
147 Leu Leu Pro Ser Thr Thr Leu Ala Pro Ala Ser Met Gly Pro
148 20 25 30
150 Ala Ala Ala Leu Leu Gln Val Leu Gly Leu Pro Glu Ala Pro Arg Ser
151 35 40 45
153 Val Pro Thr His Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg
154 50 55 60
156 Arg Arg Asp Pro Gln Glu Ala Arg Val Gly Arg Pro Leu Arg Pro Cys
157 65 70 75 80
159 His Val Glu Glu Leu Gly Val Ala Gly Asn Ile Val Arg His Ile Pro
160 85 90 95
162 Asp Ser Gly Leu Ser Ser Arg Pro Ala Gln Pro Ala Arg Thr Ser Gly
163 100 105 110
165 Leu Cys Pro Glu Trp Thr Val Val Phe Asp Leu Ser Asn Val Glu Pro
166 115 120 125
168 Thr Glu Arg Pro Thr Arg Ala Arg Leu Glu Leu Arg Leu Glu Ala Glu
169 130 135 140
171 Cys Glu Asp Thr Gly Gly Trp Glu Leu Ser Val Ala Leu Trp Ala Asp
172 145 150 155 160
174 Ala Glu His Pro Gly Pro Glu Leu Leu Arg Val Pro Ala Pro Pro Gly
175 165 170 175
177 Val Leu Leu Arg Ala Asp Leu Leu Gly Thr Ala Val Ala Ala Asn Ala
178 180 185 190
180 Ser Val Pro Cys Thr Val Arg Leu Ala Leu Ser Leu His Pro Gly Ala
181 195 200 205
183 Thr Ala Ala Cys Gly Arg Leu Ala Glu Ala Ser Leu Leu Leu Val Thr
184 210 215 220
186 Leu Asp Pro Arg Leu Cys Pro Leu Pro Arg Leu Arg Arg His Thr Glu
187 225 230 235 240
189 Pro Arg Val Glu Val Gly Pro Val Gly Thr Cys Arg Thr Arg Arg Leu
190 245 250 255
192 His Val Ser Phe Arg Glu Val Gly Trp His Arg Trp Val Ile Ala Pro
193 260 265 270
195 Arg Gly Phe Leu Ala Asn Phe Cys Gln Gly Thr Cys Ala Leu Pro Glu
196 275 280 285
198 Thr Leu Arg Gly Pro Gly Gly Pro Pro Ala Leu Asn His Ala Val Leu
199 290 295 300
201 Arg Ala Leu Met His Ala Ala Ala Pro Thr Pro Gly Ala Gly Ser Pro
202 305 310 315 320

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204 Cys Cys Val Pro Glu Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp
205 325 330 335
207 Asn Ser Asp Asn Val Val Leu Arg His Tyr Glu Asp Met Val Val Asp
208 340 345 350
210 Glu Cys Gly Cys Arg
211 355
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 27
216 <212> TYPE: DNA
217 <213> ORGANISM: Mus sp.
219 <400> SEQUENCE: 3
220 gcagccacac tcctccacca ccatgtt 27
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224 <211> LENGTH: 9
225 <212> TYPE: PRT
226 <213> ORGANISM: Mus sp.
228 <400> SEQUENCE: 4
229 Asn Met Val Val Glu Glu Cys Gly Cys
230 1 5

VERIFICATION SUMMARY

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